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Result
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Maximum Match 100
Listing first 45
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                Score
   seq length: 0
seq length: 100
                                                                                                                                                                                                                                                                                                                Query
Match
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                             987654321
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   1 tattaaggggcctggccccttaata 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/ina/1_COMB.seq:*
/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                               Length
                                                                           2006, 11:06:42; Search time 135 Seconds (without alignments) 329.178 Million cell updates/sec
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                       US-09-396-1966-86336
US-08-433-585-117
US-08-433-585-117
US-08-433-585-117
US-08-433-667-117
US-08-9439-667-117
US-08-945-909-117
US-08-945-909-117
US-08-945-909-117
US-09-396-0028-117
US-09-396-0060-117
US-09-396-196G-26177
US-08-171-389-405
US-08-171-389-405
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US-08-482-288A-405
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US-08-482-080A-405
US-08-482-080A-405
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116728,
86335, A
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
46, Appl	51, Appl	46, Appl	51, Appl	46, Appl	86391, A	86336, A	86335, A	•	8355, Ap	23652, A	245, App		1033, Ap	7211, Ap	15155, A	4, Appli	405, App	405, App	405, App	405, App

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Sequence 116728, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Mifymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US/09/396,196G
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILLING DATE: 1999-09-15;
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILLING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 116728
LENGTH: 25
TYPE: DNA
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US-09-396-196G-116728/c
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APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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Best Local &
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TITLE OF INVENTION: Methods of Genetic Analysis
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Pred. No. 17;
0; Mismatches
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEO ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 86336
LENGTH: 25
                                  ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-86336
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US-09-396-196G-86335
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US-09-396-196G-116728
   Query Match
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 1999-09-15
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TYPE: DNA
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PRIOR FILING DATE: 1998-09-17
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SOFTWARE: PastSEQ for Windows Version 4.0
EQ ID NO 116728
                                                                                                                                                                                                                                                                                              APPLICANT: Michael Mittmann
APPLICANT: David Mack
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TITLE OF INVENTION: Methods of Genetic Analysis
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David Lockhart
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89.5%;
 59.2%;
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Pred. No. 3
 Score 14.8;
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Pred. No. 1.2e+02;
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US-08-434-001-117/c
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                                                        Matches
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION NUMBER: 07/964,624
PILING DATE: 21-OCTOBER-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                    TELEFAX: (303) 793-34.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 5
NUMBER OF SEQUENCES:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPB: Diskette, 3 1/2 diskette,
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JENSEN, KIRK
APPLICANT: CHEN, HANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                      Local Similarity
                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                             TOPOLOGY:
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60
                                                        18;
                          2 ATTAAGGGGCCTGGCCCCTTAATA 25
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                                                                                                                                           H: 70 base pairs nucleic acid DEDNESS: single
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Englewood
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                                                        Conservative
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                                                                                                                                                                                                                                                                                                  Swanson
                                                                                                                                                                                                                        793-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prentice Avenue,
                                                                     57.6%;
75.0%;
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                                                                                                                                                                                                                                                                                 33,215
                                                        0;
                                                                                                                                                                                                                                                                      NEX30.3
                                                                      Score 14.4; DB 2
Pred. No. 7.3e+02
                                                      Mismatches
37
                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
                                                                                   Length 70;
                                                          Indels
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                                                        Gaps
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RESULT 6 US-08-433-585-117/c

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                                                                                                                                                                 US-08-434-425-117/c
                                                                                                                                                                                   RESULT 7
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Best Local
                                                                                                                                                 Sequence
                                                                                                                                   Patent No.
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Patent No. 5763566
                                                   APPLICANT:
APPLICANT:
APPLICANT:
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                     APPLICANT:
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APPLICATION NUMBER: US
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APPLICANT:
     TITLE OF INVENTION:
                                                                                                     APPLICANT:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
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TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
TITLE OF INVENTION: EXPONENTIAL ENRICYMENT: TISSUE
TITLE OF INVENTION: SELEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1
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                                                                                                                                   117, Application US/08434425
o. 5789157
                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                   60 AATAAGCGGCCTGGAGCTTTAACA 37
                                                                                                                                                                                                                                                                                                    l Similarity
18; Conser
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T: 8400 E. Prentice Avenue, Suite 200
Englewood
                                                                                                                                                                                                                                                                  ATTAAGGGCCCTGGCCCCTTAATA 25
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                                                                                                                                                                                                                                                                                                 57.6%; Score 14.4; DB 2; ilarity 75.0%; Pred. No. 7.3e+02; Conservative 0; Mismatches 6;
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                                  STEPHENS, ANDREW GOLD, LARRY
                                                                      MORRIS, KE
                                                                                                   JENSEN, KIRK
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21-OCTOBER-1992
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                                                                  KEVIN
 SYSTEMATIC EVOLUTION OF LIGANDS EXPONENTIAL ENRICYMENT: TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235
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Best Local
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APPLICANT:
COMPUTER READABLE FORM:
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                                COUNTRY:
                                                                                STREET:
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US-08-437-667-117/c
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Patent No. 5864026
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                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/536,428 FILING DATE: 11-JUNE-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
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             CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 57.6%;
Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Barry J. Swanson REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/964,6
FILING DATE: 21-OCTOBER-1992
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OPERATING SYSTEM:
SOFTWARE: WordPer
                                            ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                GOLD, LARRY
USA
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STEPHENS, AND
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                                                                                                                                                                                                                CHEN, HANG
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                                                                                              SELEX
235
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235
                                                                                                                             SYSTEMATIC EVOLUTION OF LIGANDS EXPONENTIAL ENRICYMENT: TISSUE
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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JS-08-437-667-117
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: NEX30.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                  CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: 07/714,131
PTITING DATE: 10-JUNE-1991
                                                                                                                                            COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordbearfect 5.1 CURRENT APPLICATION DATA:
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LENGTH: 70 base pairs
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APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 07/536,428
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APPLICATION NUMBER: 07/714,131
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                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HEILIG, JOSEPH S.
APPLICANT: GOLD, LARRY
                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: SYSTEMATIC EVOLUTION OF INVENTION: EXPONENTIAL ENRICHMENT:
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COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
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TOPOLOGY: li
                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                        CITY: Englewood
STATE: Colorado
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                                                                                                                                                                                                                                                                                                                          Swanson & Bratschun, L.L.C.
)0 E. Prentice Avenue, Suite 200
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75.0%;
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08/434,001
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Pred. No. 7
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US-08-945-909-117/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 117,
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                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US96/01
FILING DATE: 01-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,425
FILING DATE: 03-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDLIM TYPE: Diskette, 3 1/:
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
                                                                                               APPLICATION NUMBER: 08/4:
FILING DATE: 03-MAY-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/437,667
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UFILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                  FILING DATE: 03-MAY-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS TITLE OF INVENTION: ENRICYMENT: TISSUE SELEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TELECOMMUNICATION INFORMATION:
                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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Colorado
              Barry J. Swanson
ATION NUMBER: 3
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MORRIS, KEVIN
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                                                                     03-MAY-1995
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                                                                                    08/433,585
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NEX30C-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
Query Match 57.6%;
Best Local Similarity 75.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                          TELEPHONE: (303) 268-0066
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: NEX30-5/D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/434,001
FILING DATE: 05-MAY-1995
APPLICATION NUMBER: 08/906,955
FILING DATE: 05-AUGUST-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
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MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY EXPONENTIAL ENRICHMENT: TISSUE SELEX
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 8.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/396,002A FILING DATE: 14-Sep-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 1745 Shea Center Drive, Suite 330 CITY: Highlands Ranch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                    NAME: Barry J.
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(303) 793-3433
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                                                                                             DESCRIPTION: SEQ ID NO: 117:
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75.0%;
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Score 14.4; DB 3;
Pred. No. 7.3e+02;
0; Mismatches 6
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Pred. No. 7.3e+02;
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                                       DB 3;
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                                   Length 70;
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RESULT 13
PCT-US96-06060-117/c
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Sequence 117, Applicat;
Patent No. 6613526;
GENERAL INFORMATION:
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                                                                                             Sequence 117
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Best Local Similarity
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                                                                         Sequence 117, Application PC/TUS9606060 GENERAL INFORMATION:
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                     APPLICANT:
                                                         APPLICANT:
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/396,002
FILING DATE: 14-Sep-1999
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 08/434,001
FILING DATE: 05-MAY-1995
APPLICATION NUMBER: 08/95,955
FILING DATE: 05-AUGUST-1997
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
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GOLD, LARRY
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                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                         60 AATAAGCGGCCTGGAGCTTTAACA 37
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                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: NEX30-5/D
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FILING DATE: 14-Feb-2002
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                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Barry J. Swanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 80129
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CHEN, HANG
MORRIS, KEVIN
STEPHENS, ANDREW
                                                         JENSEN, KIRK
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75.0%;
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Pred. No. 7.3e+02
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                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                       Length 70
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US-09-396-196G-26177
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                                           Sequence 26177, Application US/09396196G Patent No. 6821724
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                          Query Match
   APPLICANT:
                                                                                                                                                                                                                                                                                                                         TELEFAX: (303) 793-343.
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: NEX30/PCT
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NIMBER: 08/434,001
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TITLE OF INVENTION:
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OPERATING SYSTEM: MS-DUS
OPERATING SYSTEM: MS-DUS
OPERATING SYSTEM:
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INFORMATION:
ANT: Michael Mittmann
ANT: David Mack
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                                                                                                                                                                                                            Similarity
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: Colorado
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8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                 70 base pairs
                                                                                                                                                                                                                                                                                                                                                           (303) 793-3433
                                                                                                                                                                                             Conservative
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Pred. No. 7.3e+02;
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US-08-171-389-405
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LENGTH: 25
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 3101.
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                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 27-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              FILING DATE: 17-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
          REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                              FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                              FILING DATE: 23-DEC-
PRIOR APPLICATION DATA:
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                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 22-JUN-1993
                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                REGISTRATION NUMBER:
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Turin, Lisa M.
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ore greater than or equal to the score of the result being printed,
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1: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

2: /cgn2 6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US10_NEW PUB.seq:*

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7: /cgn2 6/ptodata/2/pubpna/US10_NEW PUB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US11_NEW PUB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US11_NEW PUB.seq:*

10: /cgn2 6/ptodata/2/pubpna/US11_NEW PUB.seq3:*

11: /cgn2 6/ptodata/2/pubpna/US10_NEW PUB.seq3:*
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Match
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration
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US-10-310-914A-1153244
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-121-849-42167
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
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RESULT 2
US-10-310-914A-621697
US-10-310-914A-621697
Sequence 621697, Application US/10310914A
; Publication No. US20060003322A1
; Publication No. US20060003322A1
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US-10-310-914A-1296097/c
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CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 621697
LENGTH: 21
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SOFTWARE: PatentIn version 3:
SEQ ID NO 1296097
LENGTH: 23
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                                                                                                                                 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat Fulls OF INVENTION: Bioinformatically detectable group of novel regulatory genes TITLS OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT PEPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                     APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kyuzat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Human
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Local Similarity 100.0%;
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RESULT 3
US-10-310-914A-679212/c
; Sequence 679212, Application US/10310914A
; Publication No. US20060003322A1
; Publication No. US20060003322A1
US-10-310-914A-627249
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; ORGANISM: Human
US-10-310-914A-621697
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Best Local (
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 679219
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                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT PPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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SOFTWARE: PatentIn version 3.3
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 24
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16; Conserv
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16; Conserv
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78.9%;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                Score 15.4; DB 7;
Pred. No. 2.8e+02;
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Pred. No. 1.8e+02
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US-10-310-914A-760090/c

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                                                                                                                                                                                                                                                                                                                 RESULT 7
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; ORGANISM: Homo sapien
US-11-121-849-42167
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APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 627249
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 42167
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Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
SEQ ID NO 760090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity 78.3%;
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                  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1
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TYPE: RNA
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86.7%;
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Pred. No.
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US-11-121-849-615428/c
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US-11-121-849-615428
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                                                                                                                                         Query Match
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Best Local
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CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically
TITLE OF INVENTION: uses thereof
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CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                        TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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                                             GCCUGGCCCCCCAAUA 17
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                                                                                                             Conservative
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                                                                                                                        57.6%;
75.0%;
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                                                                                                                        Score 14.4;
Pred. No. 8
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Pred. No. 6
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Pred. No. 5.
                                                                                                           Mismatches
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US-10-310-914A-535269
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US-10-310-914A-535246
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                                                                                                                                                                                                                       Sequence 535269, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
SEQ ID NO 535269
LENGTH: 21
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LENGTH: 21
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                                                                           TITLE OF INVENTION: Bioinformatically detectable group of TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
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Publication No. US20060003322A1
                                                   NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat.
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                                      SOFTWARE: PatentIn version 3.3
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NUMBER OF SEQ ID NOS: 1388402
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US-10-310-914A-1153244
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Best Local S
Matches 15
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.020051
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1153244
LENGTH: 26
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION USES thereof
PILE REFERENCE: 06087,0200,CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOPTWARE: Patentin version 3.3
SEQ ID NO 1296097
LENGTH: 23
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
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Pred. No. 8.1e+02;
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SOFTWARE: Proprietary
SEQ ID NO 1315095
                                                                                                                                          Matches
                                                                                                                                                       Query Match 56.8%;
Best Local Similarity 63.2%;
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                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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Leake, Devin
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Sequence 4715 from Patent
CQ006075
CQ006075.1 GI:41012707
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Nucleic acids containing single nucleotide
methods of use thereof
Patent: WO 0147944-A 3548 05-JUL-2001;
Curagen Corporation (US)
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Sequence 3548 from Patent
CQ004908
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 70)
Jensen, K.B., Chen, H., Morris, K.N., Stephens, A. Systematic evolution of ligands by exponential
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Jensen, K.B., Chen, H., Morris, K.N., Stephens, A.
Systematic evolution of ligands by exponential
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Sequence 117 from patent
AR020330
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1 (bases 1 to 70)
Jensen, K.B., Chen, H.,
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Heilig,J.S. and Gold,L.
Systematic evolution of ligands by exponential
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Jensen, K.B., Chen, H.,
Systematic evolution of
                                                                                                                            Patent: US 6376474-A 117 23-APR-2002;
Gilead Sciences, Inc.; Foster City, C
                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: US 5712375-A 117 27-JAN-1998;
Location/Qualifiers
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117 from patent US 5712375.
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                                                                                       /mol_type="genomic
                                                                                                 /organism="unknown"
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enrichment:
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AY266911/c
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Matches 18
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ch 57.6%;
l Similarity. 75.0%;
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AR391734
                                                                                                                                                                                                                                              Submitted (01-APR-2003) Institute of Biology, University Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland Location/Qualifiers
                                                                                                                                                                                                                                                                                         Sigurgislason, H. and Arnason, E. Direct Submission
                                                                                                                                                                                                                                                                                                                                                    Sigurgislason,H. and Arnason,E.
Extent of mitochondrial DNA sequence variation in Atlantic cod from the Faroe Islands: a resolution of gene genealogy
Heredity 91 (6), 557-564 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gadus morhua
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Heilig,J.S. and Gold,L.
Systematic evolution of ligands by exponential
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                                                                             /note="tRNA-Thr-tRNA-Pro
                                                                                                        haplotype="S02"
country="Faroe Islands"
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/mol_type="genomic
                                                                                                                                     isolation_source="Station
db_xref="taxon:8049"
                                                                                                                                                                                                  organelle="mitochondrion"
                                                                                                                                                                                                                 organism="Gadus morhua"
                                                                                                                                                                   mol_type="genomic DNA" isolate="TFA7.04"
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Extent of mitochandrial DNA sequence variation in Atlantic the Farce Islands: a resolution of gene genealogy Haredity 91 (6), 557-564 (2003) 14560303 2 (bases 1 to 74)
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Gadus morhua isolate TPA7.08
tRNA-Thr-tRNA-Pro intergenic
AY266915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                      Sigurgislason, H. and Arnason, E.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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                                                                                                                             Acanthomorpha;
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75.0%;
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Pred. No. 1.6e+04;
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Submitted (01-APR-2003) Institute of Biology, University of
Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
Location/Qualifiers
                                                              18;
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Gadus morhua isolate TFA7.09
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus
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/mol_type="genomic DNA"
/isolate="TFA7.09"
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/db_xref="taxon:8049"
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2 (bases 1 to 74)
Sigurgislason,H. and Arnason,E.
Direct Submission
Submitted (01-APR-2003) Institute of Biology, University of Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  74
Gadus morhua isolate TFA7.11
tRNA-Thr-tRNA-Pro intergenic
AY26691B
                                                                                                                                          Sigurgislason,H. and Arnason,E.
Extent of mitochondrial DNA sequence variation in Atlantic cod from the Parce Islands: a resolution of gene genealogy
Heredity 91 (6), 557-564 (2003)
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1 (bases 1 to 74)
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Submitted (01-ARR-2003) Institute of Biology, University
Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
Location/Qualifiers
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Gadus morhua isolate TFA7.10 haplotype S03 mitochondria
CRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
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Extent of mitochondrial DNA sequence variation in Atlantic cod the Faroe Islands: a resolution of gene genealogy

Heredity 91 (6), 557-564 (2003)
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/db_xref="taxon:8049"
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haplotype S06 mitochondrial
spacer, complete sequence.
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/isolate="TFA7.11"
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/db_xref="taxon:8049"
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US-10-719-900-27015
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                       US-11-036-317-451864
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Sequence 739211,		Sequence 303549,	Sequence 295882,	Sequence 273256,	Sequence 226389,	Sequence 189638,	Sequence 227800,	Sequence 26177, A	Sequence 800772,	Sequence 255528,	Sequence 27016, A	Sequence 27015, A	Sequence 305034,	Sequence 117, App	Sequence 297112,	Sequence 134392,	Sequence 361767,	Sequence 343406,	Sequence 298920,	Sequence 263488,	

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US-10-613-390B-1/c
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CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 10/613390
PRIOR FILING DATE: 2003-07-03
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 25
TANNEL TANNE
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APPLICANT: Gene Cloning Inc
TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders
FILE REFERENCE: 60/400,137
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
                                                                                                                                                                                           APPLICANT: Gene Cloning Inc
TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders
FILE REFERENCE: 60/400,137
CURRENT APPLICATION NUMBER: US/10/613,390B
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 10/613390
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ORGANISM: artificial sequence
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RESULT 4
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                                                                      ; ORGANISM: Mus musculus
US-10-719-900-27015
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US-10-809-189-116728
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; OTHER INFORMATION: synthetic primer
US-10-613-390B-1
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Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528-1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2002-11-20

PRIOR APPLICATION UMBER: 60/427,808

PRIOR APPLICATION UMBER: 60/427,808

PRIOR PILING DATE: 2002-11-20
                                                                                                                  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 27015
LENGTH: 25
                   Query Match
Best Local (
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   Matches
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NUMBER OF SEQ ID NOS: 982914
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
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CURRENT FILING DATE: 2004-03-25
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TITLE OF INVENTION: Methods of Genetic Analysis
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                                                                                                        TYPE: DNA
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   Local Similarity 89.
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 Score 15.8; DB 8;
Pred. No. 1.4e+03;
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Pred. No. 2.
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Pred. No. 0.3;
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PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 27016
                                                                  Query Match
Best Local Similarity
Matches 17; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
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APPLICANT: David Mack
APPLICANT: David Lockhart
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TITLE OF INVENTION: Methods of Genetic Analysis
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
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                                                                                                                                                                              TYPE: DNA
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tive 0; Mismatches
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Pred. No. 1.4e+03;
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RESULT 7 US-11-036-317-189638 ; Sequence 189638, Application US/11036317 ; Publication No. US20050214823A1

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                                                                                                                                                                                                                                                                      US-11-036-317-273256
                                                                                                                                                                                                                                                                                             RESULT 9
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US-11-036-317-189638
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                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                              Sequence 273256, Application US/11036317
Publication No. US20050214823A1
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Publication No. US20050214823A1
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LENGTH: 25
SEQ ID NO 273256
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                                                    PILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
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CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
                                    PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                   TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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                SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Pred. No. 1
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Pred. No. 1.
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US-11-036-317-295882
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                                                                                                                                                                                 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 303549
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LENGTH: 25
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Best Local
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Best Local S
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                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
                                                                                                                                                                                                                                                                                                     APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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NUMBER OF SEQ ID NOS: 991174
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CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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ORGANISM: Mus musculus
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AGGAGCCTGGCCCCTTCAT 23
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Pred. No. 1.4e+03;
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Pred. No. 1
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-739211
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US-11-036-317-374272
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; ORGANISM: Mus musculus
US-11-036-317-374272
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                    Sequence 172272, Application US/11060756 Publication No. US20050221354A1
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Best Local Similarity
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
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                                                    APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
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CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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CURRENT APPLICATION NUMBER: US/11/036,317
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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89.5%;
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Pred. No. 1.
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Pred. No. 1.
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Search completed: February 7, 2006, 12:22:29 Job time: 795 secs

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                                                                                                                      US-10-719-956-370902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                 SEQ ID NO 370902
LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.2 SEQ ID NO 172272
                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                Sequence 370902, Application US/10719956 Publication No. US20040146910A1
                                                                         Best Local
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                        APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
                                                                                                                                     ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Gapop 10.0 , Gapext 1.0
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41078325 seqs, 23393541228 residues
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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AW250424 2882310.3

AZ371110 1M0122105

AZ371110 1M01231A20

AW770417 h181a12.x

AI149654 qf37c02.x

CG527767 OST106096

AW251001 2821159.3

CG524805 OST99167

CK428180 1aj11g07.

CL880134 abf42c10.

CR169973 Forward s

CG650062 OST406254

CG650062 OST406254

BX650299 Arabidops

BU812825 N001H03

CF102969 hac40a08.

CF6102969 hac40a08.
CL529021 HIV62E10.
AZ651810 1M0522O12
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CG525840 AA452589 CG573029	CG553173 AZ423820	CR131012 CD979428	BJ076360	AZ440331	AI686688	CG680849	CG538865	CW083263	AZ484117	AJ587174	AI582875	GGA350127	AA870545	CB930280	CB930280	CZ4:44284	AW250424
CG525840 OST101409 AA452589 zx39f02.s CG573029 OST204293	CG553173 OST165393 AZ423820 1M0203P22	CRI31012 Reverse s CD979428 QAG3b11.y	CRIO2161 REVEISE 8 BU076360 BU076360	AZ440331 1M0231A20	AI686688 tu35g10.x	CG680849 89M06:40	CG538865 OST129261	CW083263 104_425_1	AZ484117 1M0310N16	AJ587174 Arabidops	AI582875 ts07a07.x	AJ232133 Gallus ga	AA870545 vq23a04.r	CB930280 ri93a05.y	СВ930280 гі93а05.У	CZ444284 AE0876 Sa	AW250424 2822310.3

ALIGNMENTS

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RESULT 2
AW250424
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                                                                                                                                                            Local Similarity
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                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Enderyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enderyota; Magnoliophyta; eudicotyledons;
Enderyota; Magnoliophyta; eudicotyledons;
Enderyota; Populus.
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83 bp mRNA linear EST 15-(
N001H03 Populus bark cDNA library Populus tremula x Populus
tremuloides cDNA 5 prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                        Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupall:bhalerao@plantphys.umu.se.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from multiple libraries
Unpublished (2002)
Contact: BHALERAO RUPALI R.
                                                                                                                                                                                                                                                                                                                                                                                                               Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
The poplar tree transcriptome: Analysis of expressed sequence tags
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                                                                     ATTAAAGGGACTGGTTACTTAATA 56
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                                                                                                                                          Conservative
                                                                                                                                                                                                                              /organism="Populus tremula x Populus tremuloides"
|mol type="mRNA"
|/db_xref="taxon:47664"
|/tissue type="bark"
|/clone_Tib="Populus bark cDNA library"
                                                                                                                                                                                                                                                                                                                             . 83
                                                                                                                                                           64.0%;
79.2%;
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Pred. No.
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RESULT 3
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                           40 bp DNA linear GSS 02-OCT-201 1M0122I05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0122I05 F, genomic survey sequence.
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Plate: LLCM9 row: B column: 7
High quality sequence stop: 22.
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Email: cgapbs-r@mail.nih.gov
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Other_ESTs: 2822310.5prime`
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1 (bases 1 to 78)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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2822310.3prime NIH_MGC_7
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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AZ371110.1 GI:10484810
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                                                                                                                                                                                                                                                                                                                                                                                                     AAGGGCCTGGCCCCTTAA 23
                                                                                                                                                                                                                                                                                                                                       AAAGGCCTGGTCCCTTAA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="DHIOB (phage-resistant)"
/clone lib="NIH MGC_7"
/clone lib="NIH MGC_7"
/clone lib="NIH MGC_7"
/note="Organ: limg; Vector: pOTB7; Site 1: XhoI; Site_2: Mote="Organ: limg; Vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2822310"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8; DB 1;
Pred. No. 1.6e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 78;
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                                                                                                                                            RESULT 4
AZ371110/c
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Matches
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1 TATTAAGGGCCTGGCCCCTTAATA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss.
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Mus musculus (house mouse)
Mus musculus
                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0122 row: I column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308,
USA
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                                                        Conservative
                                                                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse_10kb plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified genomic_DNA
musculus_C57BL/6J (male) was obtained from th
Laboratory Mouse_DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="UUGC1M0122I05"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
/mol_type="genomic DNA"
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                                                                                61.6%;
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                                                        0;
                                                                                Score 15.4; DB 9;
Pred. No. 2.3e+04;
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                                                        Mismatches
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                                                                                                           Length 40;
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13 TATTATGGGTATGGGCCCATTAATA 37

AZ371110 40 k 1M0122105F Mouse 10kb plasmid clone UGC1M0122105 F, genomic AZ371110

genomic survey sequence.

d UUGCIM library Mus musculus genomic

GSS 02-OCT-2000

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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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AZ440331 83 bp DNA linear GSS 03-OCT-200 1M0231A20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0231A20 F, genomic survey sequence.
                                                                                                                                                                                                                      1 TATTAAGGGGCCTGGCCCCTTAATA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 0122 row: I column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A.,
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slam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
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'clone lib="Mouse 10kb plasmid UUGCIM library"
'note="Vector: PWD42nv, Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="UUGC1M0122I05"
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                                                                                                                                                                                                                                                                                             61.6%;
76.0%;
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                                                                                                                                                                                                                                                                                             Pred. No. 2.3e+04;
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                                                  RESULT 6
AW770417/c
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  LOCUS AW770417 98 bp mRNA linear EST 04-MAY-:
DEFINITION h181a12.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3007582
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ACCESSION
VERSION
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83
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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AZ440331.1
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Location/Qualifiers
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University of Utah
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0231 row: A column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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GGGCCTTGCCCCTTAAT 52
                                              GGGCCTGGCCCCTTAAT 24
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                                                                                               Conservative
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                                                                                                                                                                                                                 10.5 kb.range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
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94.1%;
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                                                                                                                      Score 15.4; DB 9;
Pred. No. 2.4e+04;
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RESULT 7
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qf37c02.xl Soares testis NHT
3' similar to gb:M61866 ZINC
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           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov cDNA Library Preparation: M. Bento
                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                       Homo sapiens
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prang I.M.A.G.B. Consortium DNA Sequencing by: Washington University Consortium CNA Sequencing by: Washington University
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                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                           sequence.
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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
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AW770417
AW770417.1 GI:7702459
                                                                                                                                                Hominidae; Homo.
1 (bases 1 to 64)
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National Cancer Institute, Cancer Genome Anato
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1 (bases 1 to 98)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid13"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_Site_2: NotI; Cloned unidirectionally. Primer:
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/mol_type="mRNA"
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Homo sapiens cDNA clone IMAC
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OST106096 Mus musculus 129Sv/Ev
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                                                                                                   Gene trap sequence tag generated by 3'
                                                                                                                                                                   Lexicon Genetics Incorporated 4000 Research Forest Drive, The
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                                                                   described in Zambrowicz et al
                                                                                                                                      Email: materials@lexgen.com
                                                                                                                                                                                                                                                                          Contact: Zambrowicz BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATAAGGGGTCCTGGCGTCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 1.
                               Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_testis_NHT"
/note="Vector: pT733D-Pac (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ab host="DH10B"
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78.3%;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                   (Nature.
                                                                                                                                                                      Woodlands,
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                                                               RACE from mouse ES cells as
1998 Apr 9;392(6676):608-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 64;
                                                                                                                                                                      TX 77381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA
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REFERENCE
AUTHORS
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AW251001/c
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                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLML) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. PoTy-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
                                                                                                                                                                                                                                                                                         High quality sequence stop: 10.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 73 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other_ESTs: 2821159.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ATTAAGGGCCCTGGCCCCTTAAT 24
                                                                                                                                                                                                                                                                                                                                    polyadenylated
Plate: LLCM6 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW251001
AW251001.1 GI:6593947
                                                                                                                                                                                                                                                                                                                                                                   at the beginning of the sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWZ51001 73 bp mRNA linear EST 07-JAN-2000
2821159.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821159 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.
1 (bases 1 to 73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                              ate: LLCM6 row: B column: 8
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    adaptor: GGCACGAG(G). Size-Berguing adaptor: GGCACGAG(G). Size-Berguing by
                                                                                                                                                     /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                         /clone="IMAGE:2821159"
                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="OST106096"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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78.3%;
                                                                                                                                  host="DH10B (phage-resistant)"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                     this cDNA insert was
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                                                                                       RESULT 11
CK428180/c
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CG524805/c
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KEYWORDS
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                                                     DEFINITION
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                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                         84
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94 bp mRNA linear BST 06-JAN-20 laj11g07.y1 Gastric Epithelial Progenitor 2 Mus musculus cDNA 5', mRNA sequence.
CK428180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Shu, Q., Person, C. and Sanda, A.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG524805 86 bp
OST99167 Mus musculus 129Sv/Ev I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whil kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OmniBank
Lexicon Genetics Incorporated
Lexicon Genetics Incorporated Woodlands, TX 77381, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 86)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Zambrowicz BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                 TATTAAGGGCCTGGCCCCTTAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCGGGGGCTCGCCCCTCAATA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTAAGGGGCCTGGCCCCTTAATA 25
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tom/
                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="OST99167"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                             60.0%;
78.3%;
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                                                                                                                                                                                                                                                                                                                                             Score 15; DB 10;
Pred. No. 3.8e+04,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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                                                                                        EST 06-JAN-2004
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Best Local S
Matches 18
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Contact: Jeff Gordon and Mike Lovett

Contact: Jeff Gordon and Mike Lovett

WashU, Human Generics Division

Washington University School of Medicine

lst strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified synART primers. The final CDNA was cloned in pAMPI vector in annealing reaction with Uracil DNA Glycosylase (DDG). Library
                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                             genomic, genomic survey
CL880134
CL880134.1 GI:51614669
GSS
                                                                                                                                                                                                                                                                                                                                                          CL880134 53 bp DNA abf42c10.y1 Soybean random, unfiltered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TATTAAGGGGCCTGGCCCCTTAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by Y.Korshunova and M provided by Mills JC & Gordon JI. Putative full length read vector to vector length is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L., Waterston,B. and Waters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                 Glycine max (soybean)
Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40RP from Gibco.
Location/Qualifiers
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Tidwell,R.,
                                         Nunberg, A., Bedell, J.A., Peterson, S., Jones, J., F
Methylation filtered genomic sequences from Glycine max
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dwell,R., Clifton,S.,
                                                                                               (bases 1 to 53)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="DH5alpha"
/lab_host="DH5alpha"
/clone_lib="Gastric Epithelial Progenitor 2"
/clone_lib="Gastric Epithelial Progenitor 2"
/clone_TVector: pAMP1; lst strand of cDNA was synthesized
/note="Vector: pAMP1; lst strand oligo(dT) beads, then cDNA
was amplified by PCR using modified SMART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y.Korshunova and M. Lovett. Library
materials provided by Mills JC & Gordon JI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic mice"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="Laser-captured isthmal cells from tox176"
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Pred. No. 3.8e+04;
                                            Fries, J., Budiman, M.A., N
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                                            Nguyen, H.
                                                 McMenamy,J.
guyen,H. and
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RESULT 14
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CR169973
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Best Local (
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                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                       Adams, D.J., Biggs, P.J., Cox, A.V., Jonkers, J., Smith, J., Plumb, R.W., Rogers, J. and Bradley, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR169973.1 GI:49948822
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR169973 61 bp DNA linear GSS 06-JUL-201 Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN50C03, genomic survey sequence.
CR169973 CR169973
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Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: staceyg@missouri.edu
                                                                                                                                                                  Similarity
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                                                                                                               ATTAAGGGGCCTGGCCCCTTA
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573-882-0588
                                                                                                                                                  Conservative
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/clone lib="Soybean random, unfiltered genomic library"
/clone-Type random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared
genomic DNA ranging from 0.7-1.5 kb were end repaired and
ligated to BstXI linkers prior to cloning in BstXI-cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN50c03"
                                                                                                                                                                                                                                                                                                                                   (20-FEB-2004) Sanger Centre, Hinxton, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
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                                                                                                                                                                                                                                    /clone_lib="MHPN"
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81.0%;
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Pred. No. 5.7e+04;
0; Mismatches 4
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Pred. No. 5.6e+04;
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                                                                                                                                                                                DB 11;
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Nishijima, I., Y
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Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C., and Sands, A.T.
What kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
                                                                                                                                                                                                                                                                                                                                                                                                                                         64 bp mRNA linear GSS 02-OCT-2003
OST406254 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST406254,
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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GSS.
Mus musculus (house mouse)
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Lexicon Genetics Incorporated
Lexicon Forest Drive, The Woodlands, TX 77381, USA
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                                                            Conservative
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; GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CFUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SO ID NO 150318
; LENGTH: 63
; TYPE: RNA
ORGANISM: hsa
ORGANISM: hsa
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US-11-130-645B-528520
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SEQ ID NO 528520
LENGTH: 60
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Best Local Similarity
Matches 12; Conserv
   Query Match
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TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
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NUMBER OF SEQ ID NOS: 760616
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US-11-130-645B-662769
US-11-130-645B-662743
US-11-130-645B-717754
US-11-130-645B-71779
US-11-130-645B-112090
US-11-130-645B-112090
US-11-130-645B-117452
US-11-130-645B-117452
US-11-130-645B-155510
US-11-130-645B-155510
US-11-130-645B-155719991
US-11-130-645B-179891
US-11-130-645B-179891
US-11-130-645B-17945
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US-11-130-645B-542527

US-11-130-645B-604429

US-11-130-645B-604559

US-11-130-645B-333359

US-11-130-645B-413655
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Pred. No. 3.1e+02
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US-11-130-645B-528942
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US-11-130-645B-537703
US-11-130-645B-661700
US-11-130-645B-661823
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Sequence Sequence Sequence Sequence

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117452, 155510,

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717754,

Sequence Sequence Sequence Sequence

661946 661823

662069, 662743,

Sequence Sequence

604559, 333359, 413655, 483536, 537703, 661700,

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US-11-130-645B-139002
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                                                                 Sequence 178751, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUSL3
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
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SEQ ID NO 139002
LENGTH: 64
TYPE: RNA
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GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION UNMERE: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: Patentin version 3
SEQ ID NO 178751
LENGTH: 64
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Best Local
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Best Local Similarity
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Matches 13; Conservative
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NUMBER OF SEQ ID NOS: 760616
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CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
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TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087,0202.CPUS13
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ORGANISM: hsa
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5; Mismatches 4
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Pred. No. 3.1e+02;
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Pred. No. 3
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GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION UMMBER: US/11/130,6458
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: Patentin version 3.3
SEQ ID NO 307585
LENGTH: 64
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US-11-130-645B-333006
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US-11-130-645B-178751
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CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 750616
SOPTWARE: Patentin version 3.3
SEQ ID NO 236152
                                                                  Sequence 333006, Application US/11130645B GENERAL INFORMATION:
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                  APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
   CURRENT APPLICATION NUMBER: US/11/130,645B
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13; Conser
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59.1%;
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Pred. No. 3
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Pred. No. 3
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Sequence 627039, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOPTWARE: Patentin version 3.3
SEQ ID. NO 627039
LENGTH: 64
TYPE: RNA
ORGANISM: haa
ORGANISM: haa
RESULT 11
US-11-130-645B-115601/c
; Sequence 115601, Appl
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Best Local S
Matches 13
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GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
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                                                                                                                                            Matches
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Best Local Similarity
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SEQ ID NO 333006
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NUMBER OF SEQ ID NOS: 760616
                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: hsa
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ORGANISM: hsa
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Pred. No. 3.
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Pred. No. 3.
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Pred. No. 3.1e+02;
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US-11-130-645B-235099/c
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Matches
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APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
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LENGTH: 64
TYPE: RNA
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SEQ ID NO 378454
LENGTH: 64
TYPE: RNA
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LENGTH: 64
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TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
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NUMBER OF SEQ ID NOS: 760616
SOFTWARE: PatentIn version 3
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TITLE OF INVENTION: MICRORNAS AND USES THEREOF
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Sequence 427234, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: Patentin version 3.3
SEQ ID NO 427234
TYPE: RNA
ORGANISM: hsa
US-11-130-645B-427234
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GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
FILE OF INVENTION: MICRORNAS AND USES THERBOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: Patentin version 3.3
SEQ ID NO 378526
LENGTH: 64
TYPE: RNA
GRGANISM: hsa
US-11-130-645B-378526
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Search completed: February 7, 2006, 12:30:41 Job time : 164 secs
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US-11-130-645B-427234/c
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US-11-130-645B-378526/c
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Matches 16; Conservative
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Maximum Match 100%
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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_6/ptodata/1/pna/US086_COMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ptodata/1/pna/US082_COMB.seq:*
/ptodata/1/pna/US083_COMB.seq:*
/ptodata/1/pna/US084_COMB.seq:*
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44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
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78: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
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80: /cgn2_6/ptodata/1/pna/US007COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length	DB	ID	Description
1	25	100.0	25	ا م	PCT-US03-20696-7	Sequence 7, Appli
2	25	100.0	25	53	US-10-613-390B-1	Sequence 1, Appl:
ი 3	23.4	93.6	25	۲	PCT-US03-20696-7	Sequence 7, Appli
C 4	23.4	93.6	25	53	US-10-613-390B-1	Sequence 1, Appli
ი 5	17.4	69.6		62	US-10-809-189-116728	116
	17.2	68.8		38	US-09-956-584A-366654	Sequence 366654,
	17.2		25	38	US-09-956-604-22327	Sequence 22327,
c 8	17.2	68.8	25	38	US-09-956-604A-22327	Sequence 22327,
	17.2	68.8	25	38	US-09-956-604B-22327	Sequence 22327,
_	17.2	68.8	25	77	US-60-234-049-56273	Sequence 56273,
11	17	68.0	99	24	US-09-498-485A-1998	Sequence 1998, A
12	17	68.0	99	35	US-09-912-293-44099	Sequence 44099, A
13	16.4	65.6	99	24	US-09-498-485A-4160	Sequence 4160, Ap
c 14	16.4		99	24	US-09-498-485A-4160	Sequence 4160, Ap
15	16.4		99	35	US-09-912-293-117317	Sequence 117317,
c 16	16.4	65.6	99	35	US-09-912-293-117317	Sequence 117317,
17	16.2		25	64	US-10-956-160-52224	Sequence 52224,
18	16.2	64.8	25	81	US-60-507-481-52224	Sequence 52224,
19	16.2	64.8	63	71	US-11-130-645A-561328	Sequence 561328,
20	16.2	64.8	64	71	US-11-130-645A-165370	Seguence 165370,
21	16	64.0	21	53	US-10-605-923-1462089	Sequence 1462089
c 22	16	64.0	23	49	US-10-310-914A-1296097	Sequence 1296097,
c 23	1	,)			

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RESULT 2
US-10-613-390B-1
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                                                                                                                                                             ; OTHER INFORMATION: found in any organism PCT-US03-20696-7
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          Sequence 1, Application US/10613390B
GENERAL INFORMATION:
APPLICANT: Gene Cloning Inc
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                        Matches
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: PCT/US03/20696
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: 60/400,137
PRIOR FILING DATE: 2002-08-01
    TITLE
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Oligonucleotides for Treating TITLE OF INVENTION: Proliferative Disorders FILE REFERENCE: 13552PCT
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gene Cloning, Inc.
                                                                                                                                                                                                                                          LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_signal
                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                          LOCATION: (0)...(0)
OTHER INFORMATION: found in any organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
   INVENTION: Oligonucleotides
                                                                                             1 TATTAAGGGGCCTGGCCCCTTAATA 25
                                                                                                                       25;
                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   Application PC/TUS0320696
                                                                                 TATTAAGGGGCCTGGCCCCTTAATA 25
                                                                                                                                                                                                                                                                                                                                                                                           Zhifang Zhu
Yuliang Cui
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                                                                                                                        Conservative
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US-09-975-254-1256
US-10-310-914A-621697
US-10-604-926-35057
US-10-605-923-550465
US-10-605-923-987120
US-10-605-923-1481673
US-10-605-923-1481673
US-10-707-975B-361066
US-10-719-900-2701.6
US-10-719-900-2701.6
US-10-719-900-2701.6
US-10-719-900-2701.6
US-10-719-900-2701.6
US-10-719-900-2701.6
US-10-719-900-2701.6
US-11-036-317-226389
US-11-036-317-295882
US-11-036-317-295882
US-11-036-317-395882
                                                                                                                       0
                                                                                                                                Score 25;
Pred. No.
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                                                                                                                       Mismatches
  for Treating Proliferative
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27015, A
27016, A
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1256, Ap
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US-10-613-390B-1/c
Sequence 1, Application US/10613390B
GENERAL INFORMATION:
APPLICANT: Gene Cloning Inc
TITLE OF INVENTION: Oligonucleotides for Treating
FILE REFERENCE: 60/400,137
CURRENT APPLICATION NUMBER: US/10/613,390B
CURRENT FILING DATE: 2003-07-03
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GENERAL 1
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Best Local
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Proliferative Disorders

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; OTHER INFORMATION: found in any organism PCT-US03-20696-7
                                                                                                                                                                                                                                                                                           APPLICANT: Zhi Wang
TITLE OF INVENTION: Oligonuclectides for Treati
TITLE OF INVENTION: Proliferative Disorders
TILE REFERENCE: 13552PCT
CURRENT APPLICATION NUMBER: PCT/US03/20696
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: 60/400,137
PRIOR FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: synthetic primer US-10-613-390B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US03-20696-7/c
                                      Query Match
Best Local Similarity
Matches 24; Conserv
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 25
TENGTH: 25
                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 7
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CURRENT APPLICATION NUMBER: US/10/613,390B
CURRENT FILING DATE: 2003-07-03
                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gene Cloning,
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                                                                                                                                                  OTHER INFORMATION: found
                                                                                                                                                                          NAME/KEY: misc_signal
                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                      24; Conservative
1 TATTAAGGGGCCTGGCCCCTTAATA
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Yuliang Cui
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                                                    93.6%;
                                                                                                                                                  in any organism
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Pred. No. 5.1
0; Mismatches
                                                     Score 23.4;
Pred. No. 25;
                                        Mismatches
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OTHER INFORMATION: synthetic primer US-10-613-390B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-809-189-116728
PRIOR APPLICATION NUMBER: 60/234,017
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 36654
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
S-09-956-584A-366654
                                                                                                                                                                                                      Sequence 366654, Application US/09956584A
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Genetic Analysis of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
LENGTH: 25
TYPE: DNA
ORGANISM: artificial sequence
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 116728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 116728, Application US/10809189 GENERAL INFORMATION:
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/956,584A CURRENT FILING DATE: 2001-09-19
                                                                                                                                                                                          FILE REFERENCE: 3115.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 25
TYPE: DNA
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94.7%;
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96.0%;
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Pred. No. 2
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US-09-956-604B-22327/c ; Sequence 22327, Application US/09956604B ; GENERAL INFORMATION:
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Sequence 22327, Application US/09956604A
; GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; Escherichia coli US-09-956-604A-22327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-956-604-22327/c

; Sequence 22327, Application US/09956604

; GENERAL INFORMATION:
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LENGTH: 25
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Best Local
CURRENT APPLICATION NUMBER: US/09/956,604B
               APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3117.1
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/956,604A CURRENT FILING DATE: 2001-09-19 PRIOR APPLICATION NUMBER: 60/234,049 PRIOR FILING DATE: 2000-09-19
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CURRENT FILING DATE: 2001-99-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe S
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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TITLE OF INVENTION: Methods of Genetic Analysis
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ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25
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86.4%;
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Pred. No. 1.
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Pred. No. 1.2e+04;
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                               of Escherichia coli
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; ORGANISM: Escherichia coli
US-09-956-604B-22327
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                                                                                                                                                                                APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO46
CURRENT APPLICATION NUMBER: US/09/498,485A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/118,775
PRIOR FILING DATE: 199-02-05
NUMBER OF SEQ ID NOS: 8166
SEQ ID NO 1998
                                                                                                                                                                                                                                                                                                                                                Sequence 1998, Application US/09498485A GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/60/234,049
CURRENT FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTMARE: FastSEQ for Windows Version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Eschericia coli
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank U00096
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TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Escherichia coli
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PRIOR FILING DATE: 2000-09-19
                   NAME/KEY: misc_feature
LOCATION: (39)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (61)
                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                 TYPE: DNA
                                                                                                                                                                  ENGTH: 99
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INFORMATION: n equals a,t,g, or
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Pred. No. 1.2e+04
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 44099
LENGTH: 99
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CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 08/103,744
PRIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 08/196,363
PRIOR FILING DATE: 1994-02-15
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PRIOR FILING DATE: 1999-02-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/221,623
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                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: (39)..(39)
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
                                 OTHER INFORMATION: n is
                                                    NAME/KEY: misc_feature LOCATION: (73)..(73)
                                                                                                       OTHER INFORMATION: n is
                                                                                                                              NAME/KEY: misc_feature
LOCATION: (66)..(66)
                                                                                                                                                              FEATURE
                                                                                                                                                                           LOCATION: (61)..(61)
OTHER INFORMATION: n is
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LOCATION: (98)
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LOCATION: (73)
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LOCATION: (66)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/741,830 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/813,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1994-03-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/196,362
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Pred. No.
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US-09-498-485A-4160/c
Sequence 4160, Application US/09498485A; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
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                                                            RESULT 14
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US-09-498-485A-4160
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; OTHER INFORMATION: n
US-09-912-293-44099
                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/498,485A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/118,775
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 8166
SEQ ID NO 4160
LENGTH: 99
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO46
                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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JOCATION: (25)
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                                                                                                                                                                        Local
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                                                                                                                                                           Similarity
17; Conserv
                                                                                                                             TATTAAGGGCCTGGCCC 18
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Pred. No. 2.
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Pred.
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1.6e+04;
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RESULT 15
US-09-912-293-117317
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PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 8166
SEQ ID NO 4160
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 08/103,774
PRIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                                            APPLICANT: Rosen,
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                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/249,651
                                                                                                                                                                                                                                                            FILE REFERENCE: PO-100
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Genes, Sequences,
                                                                                                                                  PRIOR APPLICATION NUMBER: 08/104,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Genes, Sequences, FILE REFERENCE: PO46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: (92)
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OTHER INFORMATION: n equals
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                                                                                FILING DATE: 1993-08-09
APPLICATION NUMBER: 08/196,363
FILING DATE: 1994-02-15
                              APPLICATION NUMBER: 09/859,490 FILING DATE: 2001-05-18 APPLICATION NUMBER: 08/196,362
                 FILING DATE:
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NUMBER: 08/221,623
              1994-02-15
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Pred. No. 2.8e+04;
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Search completed: February 7, 2006, 12:27:52 Job time : 3631 secs
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PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 09/741,830
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR FILING DATE: 2001-03-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 117317
LENGTH: 99
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                Query Match 65.6%; Score 16.4; DB 35; Best Local Similarity 94.4%; Pred. No. 2.8e+04; Matches 17; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: misc_feature
LOCATION: (92)..(92)
OTHER INFORMATION: n is equal to a,t,g, or c
-09-912-293-117317
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LOCATION: (8)...(8)
OTHER INFORMATION: n is equal to a,t,g, or c
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THER INFORMATION: n is equal to a,t,g, or c
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OCATION: (71)...(71)
THER INFORMATION: n is equal to a,t,g, or c
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OCATION: (29)..(29)
THER INFORMATION: n is equal to a,t,g,
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WHER INFORMATION: n is equal to a,t,g, or c
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OCATION: (19)..(19)
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OCATION: (25)..(27)
                                                                                           43 TÁTTAAGGGGCCCGGCCC 60
                                                                                                                                    1 TATTAAGGGGCCTGGCCC 18
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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seq length: 100
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Gapop 10.0 , Gapext 1.0
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25
1 tattaaggggcctggccccttaata
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11:
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

19 14	C 18 14	17 14	c 16 14	15 14	C 14 14	13 14		11 14	14	9 14	8 14.2	C 7 14.4	6	c 5 15	C 4 15	c 3 15	c 2 23.4	–	No. Score	Result		
.2 56.8	.2 56.8	.2 56.8	.2 56.8	.2 56.8	.2 56.8	.2 56.8	.2 56.8	.2 56.8	56	56	56	57	15 60.0	.4 61.6	.4 61.6	.8 63.2	.4 93.6	25 100.0	;	Query	٠,	
51 4	49 1	49 1	49 6	49 6	49 2	49 2	49 2		49 2	49 2	31 3	70 2	90 1	50 4	50 4	51 4	25 1	25 1	Match Length DB			
AAL30340	2 ADE80435	2 ADE80435	ABK82896	ABK82896	AAX17405	AAX17405	AAT64117	AAT64117	AAQ69655	AAQ69655	AAA78645	AAT71443	4 ACL62385	AAL31507	AAL31509	AAL30340	2 ADK67857	2 ADK67857	ID			SUMMARIES
Aal30340 Human SNP	Ade80435 Duplex ol	Ade80435 Duplex ol	Abk82896 DNA bindi	Abk82896 DNA bindi	Aax17405 Test sequ	Aax17405 Test sequ	Aat64117 Human ade		Aaq69655 Human ade	Aaq69655 Human ade	Aaa78645 Human gen	Aat71443 Glioblast	Acl62385 Human col	Aal31507 Human SNP	Aal31509 Human SNP	Aal30340 Human SNP	Adk67857 Transcrip	Adk67857 Transcrip	Description			

The present sequence is that of oligo #2,

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25-mer single-stranded

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Example 21; SEQ ID NO 7; 36pp; English.

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24440 04 04 04	2 4 4 4 4 8 112 112 112 112 112 112 112 112 112 1
AAC11080 AAI27785 ABA7696 ABA7696 ABS24470 ABS24446 ADJ95320 ADZ11539 AAF61993 ABL95768 ADB957044 ADM87895 ADM87895	AAX04573 AAZ11454 ADD94048 ADD94058 ACK17136 ACK17136 ACK17737 ADK17981 ADK17982 ADK59933 ADK59933 ADJ53934 ABT34022 AAJ31509 AAL31509 AAL31509 AAL31507 AAL31509
Aacilloo Human sec Aai27785 Probe #17 Aba76096 Human foe Aak24770 Human bra Abs24246 Human gen Adj95320 Novel NOV Adz11539 Human col Aaf61993 K. marxia Ab195768 Rat GALP- Add677044 Mouse Gal Adm87895 Gene expr Adz27716 Chemosens	PCR px Wild-t 8 PCR p 8 PCR p Human Human 1 Satux 2 Satux 2 Satux 3 Site 4 Site Human Human Human Human

ALIGNMENTS

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RESULT 1
ADK67857
ID ADK6
XX
AC ADK6
XX
Treating a proliferative disorder in a subject comprises administering proliferation-inhibiting amount of a single-stranded oligonucleotide capable of binding to one or more DNA-binding proteins or RNA primers ithe subject.
                                                                                                                    Zhu
                                                                                                                                                                                                                                                                                                                                GC_signal
                                                                                     WPI; 2004-156997/15.
                                                                                                                                                                                     01-AUG-2002; 2002US-0400137P
                                                                                                                                                                                                                      30-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription activator-binding oligonucleotide (oligo #2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK67857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK67857 standard; DNA; 25 BP
                                                                                                                                                                                                                                                     12-FEB-2004.
                                                                                                                                                                                                                                                                                     WO2004012654-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                     (GENE-) GENE CLONING INC.
                                                                                                                                                                                                                                                                                                                                                                     TATA_signal
                                                                                                                    Cui Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       lung cancer; melanoma; leukaemia; gene therapy; ss.
                                                                                                                                                                                                                      2003WO-US020696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                    Li L,
                                                                                                                    Wang Z;
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RESULT 2
ADK67857/c
ID ADK678
XX ADK678
XX ADK678
XX ADK678
XX Cytost
XX Cytost
XX Synthe
XX Synthe
XX Synthe
XX MO2004
XX I2-FEB
XX MO2004
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XX I2-FEB
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Best Local S
Matches 25
                    The present sequence is that of oligo #2, a 25-mer single-stranded oligonucleotide that includes a TATA signal and GC signal sequence. Oligonucleotide in a claimed method of modulating transcription in a cell. The invention provides compositions and methods for treating a proliferative disorder, in particular lung cancer, melanoma or leukaemia (claimed),
                                                                                                                                                                                                                                              proliferation-inhibiting capable of binding to one the subject.
                                                                                                                                                                                                                                                                      Treating a proliferative disorder in a subject comprises administering proliferation-inhibiting amount of a single-stranded oligonucleotide capable of binding to one or more DNA-binding proteins or RNA primers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising administering a proliferation-inhibiting amount of a single-stranded oligonucleotide that is capable of binding to one or more DNA-binding proteins or RNA primers. In an example from the invention, mice were administered p388 leukaemia cancer cells by i.p. injection and then received i.v. injections of oligo #2 and/or oligo #4 (a 7-mer random oligo DNA). Results showed that oligo #2 and dosage of 1 mg/kg/day i.v. with oligo #4 at 1 mg/kg/day i.v. attained perfect results, up to 36 days after cancer cell injection, with a 100% survival rate. The 7-mer alone attained a 60% survival rate. The results showed that oligo #2 could
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-2002; 2002US-0400137P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2003; 2003WO-US020696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GC_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription activator-binding oligonucleotide (oligo #2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK67857 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #2 is used in a claimed method of modulating transcription in a cell. The invention provides compositions and methods for treating a proliferative disorder, in particular lung cancer, melanoma or leukaemia (claimed),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004012654-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic;
                                                                                                                                                                                          Example 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATA_signal
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                                                                                                                                                                                                                                                                                                                                                                                          2004-156997/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENE CLONING INC.
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Ding
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7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Pred.
                                                                                                                                                                                             English
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n in a cell. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
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7-mer alone
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administering

proliferation-inhibiting

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RESULT 3
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apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interferons, interferons interferons such protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the present of diseases them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stranded oligonucleotide that is capable of binding to one or more DNA-binding proteins or RNA primers. In an example from the invention, mice were administered p388 leukaemia cancer cells by i.p. injection and then received i.v. injections of oligo #2 and/or oligo #4 (a 7-mer random oligo DNA). Results showed that oligo #2 at a dosage of 1 mg/kg/day i.v. with oligo #4 at 1 mg/kg/day i.v. attained perfect results, up to 36 days after cancer cell injection, with a 100% survival rate. The 7-mer alone attained a 60% survival rate. The results showed that oligo #2 could interfere with RNA transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement related protein; cytochrome; kinesin; cytokine; interleukin; G-protein coupled receptor; thioesterase; inf multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer. amyloid protein; angiopoietin; apoptosis related protein; cadherin; cytolin; polymerase; oncogene; histone; kinase; colony stimulating factoryclin; polymerase; oncogene; histone; kinase; cytokine; interferon;
                                                                                                                            The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoiet
                                                                                                                                                                             Claim
                                                                                                                                                                                                                         oncogenes and
                                                                                                                                                                                                                            Polymorphic nucleic acids encoding oncogenes and histones, useful for
                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL30340 standard;
                                                                                                                                                                                                             autoimmune
                                                                                                                                                                                                                                                                                                                                                                      28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2000; 2000WO-US035498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous
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                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
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                                                                                                                                                                           1; Page 2404; 4143pp;
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                                                                                                                                                                                                                                                                                                           Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
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                                                                                                                                                                                                           useful for infections.
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RESULT 4
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proteins, cytochromes, kinesins, cytokines, interferons, interleukins, (protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                      The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related
                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets
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27-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and autoimmune diseases and infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0173419P.
2000US-00173419.
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cc are differentially expressed in colon cancer cells. The invention also color relates to vectors and host cells comprising a differentially expressed cc polynucleotide of the invention; a method for detecting a cancerous cell cc inhibiting a cancerous phenotype of a cell by inhibiting a gene product of the polynucleotides; a method for cell by inhibiting a gene product of the polynucleotides; a method of treating an individual with cancer by cand an isolated antibody that specifically binds to a polypuble encoded cc by one of the 9672 polynucleotides. The polynucleotides, polypuble encoded cc of the diagnosis, prognosis and management of cancer; for the cc identification of agents that modulate the phenotype of cancerous cells; for the identification of cancer, especially colon cancer and metastasized colon cancer, but also breast or pancreatic cancer. The polynucleotides can elso useful as a source of probes or primers for use in diagnostic responses for the grevention or treatment of cancer. The present sequence crepresents a specifically claimed polynucleotides or their encoded concerns and metastasized colon cancer the prevention or treatment of cancer. The present sequence crepresents a specifically claimed polynucleotide which is differentially expressed polynucleotide printed printed specification, but was obtained in colon cancer. Note: The sequence data for this patent did cor tep. wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotides, which are cancer cell, useful for treating cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to 9672 polynucleotides (ACL53866-ACL63537) which differentially expressed in colon cancer cells. The invention also
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03-MAY-1995;
03-MAY-1995;
03-MAY-1995;
                                                                                                           The present sequence is a single stranded DNA ligand to the human brain tumour derived, glioblastoma U251 cell line, prepared by systematic evolution of ligands by exponential enrichment (SELEX). A single stranded DNA pool was incubated with U251 cells, and the tighter binding sequences partitioned from the rest of the pool by filtering the reaction through nitrocellulose filters. Twenty rounds of selection were carried out, using a decreasing concentration of U251 cells as the SELEX progressed. Ligands to glioblastoma cell lines can be used in vivo to image glioblastomas, and for the therapeutic localisation of the ligand or the therapeutic localisation of the ligand or
                                                                                                   glioblastomas, other attached
                                                                                                                                                                                                                                                                              Identifying nucleic acid ligands for tissues - by mixt. of nucleic acids with tissue and enriching i
                                                                           Sequence
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systematic evolution of ligands
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95US-00434001.
95US-00434425.
95US-00437667.
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                                                                                                    agents
                          0;
                                                                           14 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour; SELEX; in vivo; imagir
nds by exponential enrichment;
                                         Score 14.4;
Pred. No. 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15;
                          Mismatches
                                                                                                                                                                                                                                                                                                                                              Stephens A,
                                                                           25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
1.5e+03;
                                                   DB
                                                   2
                                                                                                                                                                                                                                                                                                                                               Go1d
                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 90
                                                   Length
                                                                                                                                                                                                                                                                                  y contacting candidate for increased affinity
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        imaging;
hment; cancer;
                                                     70;
                           0,
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                             Gaps
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                             0
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B

60

AATAAGCGGCCTGGAGCTTTAACA 37

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RESULT 9
AAQ69655
ID AAQ6
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                                                                                                                                                                                                                                                                                                cc base, or the complement of the segment. Also described are: (1) an allele compensation of the segment. Also described are: (1) an allele capacitic oligonucleotide that hybridises to a segment of the novelty; (CC (2) an isolated nucleic acid comprising a sequence of the novelty where CC the polymorphic site within the sequence is occupied by a base other than CC the reference base indicated in the specification; and (3) analysing a concleic acid, comprising obtaining a nucleic acid from an individual, and determining a base occupying any one of the polymorphic sites of the covelty. The nucleic acid segments and method can be used to analyse an CC individuals nucleic acid segments and method can be used to analyse an CC individuals nucleic acid sequences for the presence of polymorphisms. The compression of the phenotype with a particular polymorphism. The presence of polymorphic sites are useful for, e.g. forensics, paternity testing, CC correlation of polymorphisms with phenotypic traits and for genetic correlation of polymorphisms with phenotypic traits and for genetic correlation of polymorphisms with phenotypic traits and for senetic correlations of human genomic DNA fragments containing polymorphic sites. The base occupying the polymorphic site is indicated using IUPAC-IUB
                                                                                                                                                                               Matches
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                       Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a nucleic acid segment of 10-100 contiguous bases chosen from one of 632 fragments (AAA78631 to AAA79262), where the segment comprises a polymorphic site or an immediately adjacent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 5; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             testing, genetic mapping,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500198/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patil N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JAN-2000; 2000EP-00250023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phenotypic trait; genetic analysis; genetic mapping; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; genomic DNA; polymorphism; hybridisation; polymorphic site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA78645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA78645 standard; DNA;
                                                                                                                                                                                                  Local
                                                                                                                                                                               16;
                                                                                                                                                                                              Similarity
                                                                                                                            TATTAAGGGGCCTGGCCCCTT 21
                                                                                                       TCTTCAGRGGACTGGCTCCTT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shah N,
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                     BP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA polymorphic site sequence tag SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00238402.
                                                                                                                                                                                                                                                   A; 8 C; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warrigton
                                                                                                                                                                                            56.8%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>3</u>1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site; forensic;
                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                   G; 11 T; 0 U; 1 Other;
                                                                                                                                                                                          Score 14.2; DB 3; Pred. No. 3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome; allele-specific; primer;
                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               paternity
                                                                                                                                                                             4
                                                                                                                                                                                                             Length 31;
                                                                                                                                                                             Indels
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AAQ69655 standard; DNA; 49

RESULT 10
AAQ69655/c
ID AAQ696
XX
AC AAQ696
XX

standard;

DNA; 49

25-MAR-2003 01-MAR-1995 AAQ69655; AAQ69655

(revised)
(first entry)

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10 7 Matches Query Match Best Local

l Similarity 16; Conserv

Conservative

0;

56.8%;

Score 14.2; Pred. No. 3. Mismatches

.5e+03

DB 2;

Length 49;

Indels

0

Gaps

0

GGGGCCTGGCCCCTTAATA 25 GGGGCCCGGCCCGTTAAGA 28

Sequence

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CC of synthetic or biological cpds. for their ability to bind DNA test
CC sequences. The assay is versatile in that any number of test sequences
CC can be tested by placing the test sequence adjacent to a defined protein-
CC binding screening sequence. Binding of mols. to these test sequences
CC changes the binding characteristics of the protein mol. to its cognate
CC changes the binding characteristics of the protein mol. to its cognate
CC could be tested by placing the complexes is disturbed, generating changes
CC cquilibrium of the DNA:protein complexes is disturbed, generating changes
CC cquilibrium of the DNA:protein complexes is disturbed, generating changes
CC to eucaryotic general transcription factors (e.g. TFIID), where the
CC target region is typically selected from DNA sequences adjacent to the
CC target region is typically selected from DNA sequences adjacent to the
CC thinding site for the eucaryotic transcription factor. Numerous exemplary
CC test sequences are given: the sequences in AAQ69551-731 and AAQ69850
CC correspond to promoter trapets (typically, TATA box-contg. sites) for
CC thuman genes and the sequences in AAQ69732-849 correspond to promoter
CC targets for viral genes. The test sequences may also be randomly
CC generated. DNA:protein interaction may be used for sccreening purposes,
CC e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see
CC AAQ69851-52, AAQ69865 and AAQ69891). (Updated on 25-MAR-2003 to correct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                         A DNA protein-binding assay is provided,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; Page 414; 587pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as molecular reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-directed DNA-binding molecules - useful in pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edwards CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1992;
17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9 transcription factor; TFIID: ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenosine deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ69655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENELABS TECHNOLOGIES INC
  49
BP; 6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cantor CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-00996783.
93US-00123936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-US012388
16 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andrews BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene,
24 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Turin LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region.
                                                                                                                                                                                                                                                                                                                                                                                                                              useful for screening libraries
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RESULT 11
AAT64117
ID AAT64
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AAC AAT64
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DT 25-MA
DT 17-MA
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DE Humar
XX
Duple
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                                                                                                                                                                                                                                                                                                                                                                                             CC of synthetic or biological cpds. for their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences come be tested by placing the test sequence adjacent to a defined protein-cc binding screening sequence. Binding of mols. to these test sequences changes the binding characteristics of the protein mol. to its cognate coinding sequence. When such a mol. binds the test sequence, the containing sequence of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe. One application of this method is couraryotic general transcription factors (e.g. TFIID), where the cut arget region is typically selected from DNA sequences adjacent to the binding site for the eucaryotic transcription factor. Numerous exemplary cut set sequences are given: the sequences in AAQ69251-731 and AAQ69850 correspond to promoter targets (typically, TATA box-contg. sites) for thangets for viral genes. The test sequences may also be randomly constructed. DNA:protein interaction may be used for screening purposes, cap. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see CAAQ69851-52, AAQ69865 and AAQ69891). (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-directed DNA-binding molecules - useful in pharmaceuticals and
Duplex DNA; target region; binding characteristic; DNA binding protein;
                                                                                                                                                                                                                                                                                                                                                      Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as molecular reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                 Human adenosine
                                                               25-MAR-2003
17-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A DNA protein-binding assay is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edwards CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1992;
17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adenosine deaminase
                                                                                                              AAT64117;
                                                                                                                                              AAT64117 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA protein-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    target;
                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                        1 TATTAAGGGGCCTGGCCCC 19
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA box;
                                                                                                                                                                                                                            TCTTAACGGCCGGGCCCC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 414; 587pp; English
                                                                                                                                                                                                                                                                                                                                                      BP; 6 A;
                                                                                                                                                                                                                                                                                          Conservative
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(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-00996783.
93US-00123936.
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                               deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ng assay, test sequence, screening sequence, promoter, Herpes Simplex Virus, HSV, origin of replication, UL9, tor, TFIID: ds.
                                                               entry)
                                                                                                                                                                                                                                                                                                       56.8%;
                                                                                                                                                                                                                                                                                                                                                      16 C; 24 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews BM,
                               gene TFIID binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene,
                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                      Score 14.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              provided, useful for screening libraries
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  target region
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                                                                                                                                                                                                                                                                                                       DB 2;
.5e+03;
                                                                                                                                                                                                                                                                                                                      Length 49
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                                                                                                                                                                                                                                                                                          Indels
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RESULT 12
AAT64117/c
ID AAT641
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAT63713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for altering the binding characteristics of a DNA-binding protein to duplex DNA comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small molecule is bound to the target region, it is adjacent to, but not overlapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding of the small molecule may inhibit or enhance the binding the small molecule may inhibit or enhance the binding the small molecule may inh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for different DNA sequences. The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also AAT49539- 74). (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the DNA-binding protein to its binding site. The compounds isolated using this method are potentially useful as therapeutic agents for treatment of any disease which involves a specific DNA sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altering binding characteristics of DNA binding proteins to duplex DNA -by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer etc.
                                                                    Human adenosine
                                                                                                                         25-MAR-2003
17-MAR-1997
                                                                                                                                                                                                                                                AAT64117 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; ds.
                                                                                                                                                                                                AAT64117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-020402/02.
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23-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Turin LM,
                                                                                                                                                                                                                                                                                                                                                                            GGGGCCCGGCCCGTTAAGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                      (revised)
(first entry)
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92US-00996783.
93US-00123936.
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                                                                    deaminase gene TFIID binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews BM, Cantor CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.8%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 C; 24 G; 3
                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                  ₽₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length
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Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer;

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RESULT 13
AAX17405
ID AAX17
XX AAX17
XX AAX17
XX AAX17
XX O6-MA
XX Test
XX Test
XX Tucle
XX Tucle
XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                     CC sequence-specifically to a target region, where, when the small molecule CC is bound to the target region, it is adjacent to, but not overlapping by CC more than 4 bp, a binding site for a DNA-binding protein. The small CC the DNA binding protein, pref. TFIID, to its binding site on the binding of CC the DNA-binding protein, pref. TFIID, to its binding site on the duplex CC DNA. The binding protein to its binding site or enhance the binding of the DNA-binding protein to its binding site. The compounds isolated CC using this method are potentially useful as therapeutic agents for CC cancer, or inherited genetic disorders etc. The method is sultable for CC cancer, or inherited genetic disorders etc. The method is sultable for CC cancer by a sequence of the compounds isolated CC concer. On the sequences. The design of those duplex DNA's allows a cCC specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also AAT49539-74). (Updated on 25-MAR-2003 to CC correct PF field.)
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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23-DEC-1992;
17-SEP-1993;
Homo sapiens
                             Test sequence; DNA-binding molecule; screening sequence; human; nucleic acid amplification; target; viral; ds.
                                                                               Test sequence from human adenosine deaminase gene
                                                                                                               06-MAY-1999
                                                                                                                                                  AAX17405
                                                                                                                                                                                 AAX17405 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           target regions in the method of the invention. The second to duplex DNA the binding characteristics of a DNA-binding protein to duplex DNA the binding characteristics of a DNA with a small molecule which binding characteristics of a DNA with a small molecule which binding characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Col 305-306; 264pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altering binding characteristics of DNA binding proteins to duplex DNA -
by attaching specific small cpd. to target region close to the protein's
binding site, useful in treatment of viral disease, cancer etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-020402/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inherited genetic disorder; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENELABS TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                             .TATTAAGGGGCCTGGCCCC 19
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                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                               (first entry)
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92US-00996783.
93US-00123936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in AAT63713-4312 represent duplex DNA's which act a
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                                                                                                                                                                                                                                                                                                                                               56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                   16 C;
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                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                               Length 49;
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                                                                                                                                                                                                                                                                                                                                 Gaps
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PXXXXXXX
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                                 and where the mixture of duplex DNA test oligonucleotides includes several test sequences; (ii) incubating the test molecule, the mixture of duplex DNA test oligonucleotides and the DNA-binding protein for a time sufficient to permit binding of the test molecule to test sequences in the duplex DNA; (iii) separating unbound test oligonucleotides from test oligonucleotides bound to binding protein; (iv) amplifying the unbound test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and (vi) sequencing the isolated test oligonucleotides. Test sequences AAX17001-X17481 and AAX17600 correspond to promoter targets for human genes and test sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1992;
17-SEP-1993;
20-DEC-1993;
Sequence 49
                                                                                                                                                                                                                                                             having a test sequence adjacent to a screening sequence, where the screening sequence binds to the DNA-binding protein with a binding affinity that is independent of the DNA sequence of the test sequence,
                                                                                                                                                                                                                                                                                                                      Sequences AAX17001 to AAX17600 represent specifically claimed target test sequences that are used in the method of the invention of determining the DNA sequence preference of a DNA-binding molecule. The method comprises:

(i) adding a test molecule and a DNA-binding protein to a mixture of duplex DNA test oligonucleotides, each of the test oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of DNA sequence preference of a DNA-binding molecule -based on inhibition of binding of protein to oligonucleotide sequence attached to test sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Col 307-308; 270pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fry KE,
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BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;
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93US-00123936.
93US-00171389.
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                               Query Match
Best Local S
Matches 16
                                16;
               7
                                       Similarity
              GGGCCTGGCCCCTTAATA
                                Conservative
                                       56.8%;
                                0
               25
                                Score 14.2; DB 2;
Pred. No. 3.5e+03;
0; Mismatches 3
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                                               Length 49;
                                Indels
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                                Gaps
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AAX17405/c
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09-FEB-1999
                                    US5869241-A.
                                                                                                                    Test sequence; DNA-binding molecule; screening sequence; human; nucleic acid amplification; target; viral; ds.
                                                                                                                                                                                                                         06-MAY-1999
                                                                                                                                                                                                                                                                    AAX17405
                                                                                                                                                                                                                                                                                                             AAX17405 standard; DNA; 49
                                                                             Homo sapiens
                                                                                                                                                                                  Test sequence
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                  from human adenosine deaminase gene
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BX BX SX XX XX X BX BX XX XX

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ABK82896
ID ABKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAX17001 to AAX17600 represent specifically claimed target test cequences that are used in the method of the invention of determining the CDNA sequence preference of a DNA-binding molecule. The method comprises: (1) adding a test molecule and a DNA-binding protein to a mixture of duplex DNA test oligonuclectides, each of the test oligonuclectides having a test sequence adjacent to a screening sequence, where the screening sequence binds to the DNA-binding protein with a binding caffinity that is independent of the DNA sequence of the test sequence, and where the mixture of duplex DNA test oligonuclectides includes several test sequences; (ii) incubating the test molecule, the mixture of duplex DNA test oligonuclectides and the DNA-binding protein for a time sufficient to permit binding of the test molecule to test sequences in the duplex DNA; (iii) separating unbound test oligonuclectides from test oligonuclectides bound to binding protein; (iv) amplifying the unbound test oligonuclectides; (v) repeating steps (ii) to (iv); (vi) isolating these oligonuclectides; (v) repeating steps (ii) to (iv); (vi) isolating correspond to promoter targets for human genes and test sequences axx17600 correspond to promoter targets for viral genes
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Best Local
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23-DEC-1992;
17-SEP-1993;
20-DEC-1993;
                                                                                                             DNA binding molecule screening; inhibition of transcription; infection; human immunodeficiency virus; HIV; parasite; cancer; cardiovascular; respiratory; gastrointestinal; endocrine; metabolic; rheumatic; immunological; haematological; neurological; psychiatric; dermatological; ophthalmological; musculo-skeletal; urogenital disorder; ss.
                07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                US6384208-B1
                                                                                Synthetic.
                                                                                                                                                                                                                     DNA binding molecule screening method test sequence #405.
                                                                                                                                                                                                                                                                                           ABK82896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Col 307-308; 270pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of DNA sequence preference of a DNA-binding molecule -based on inhibition of binding of protein to oligonucleotide sequence
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                                                                                                                                                                                                                                                                                                                           ABK82896 standard; DNA; 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                       (first entry)
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92US-00996783.
93US-00123936.
93US-00171389.
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Pred. No. 3.5e+03;
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Job time :

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Search completed: February

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Best Local S
Matches 16
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23-DEC-1992;
17-SEP-1993;
20-DEC-1993;
07-JUN-1995;
                                                                                                                                                           parasites), cancer, cardiovascular, respiratory, gastrointestinal, endocrine/metabolic, rheumatic/immunological, haematological, musculo-neurological, psychiatric, dermatological, ophthalmological, musculo-skeletal, genetic or urogenital disorders. The method provides sequence-specific inhibition of transcription of pathological genes without affecting transcription of cellular genes regulated by the same transcription factor, and can be applied to regulation of any gene. ABK82492-ABK83155 represent DNA binding molecule test sequences used the method of the invention
                                                                                                                                                                                                                                                                                                            The invention relates to a method of decreasing transcriptional activity in a duplex deoxyribonucleic acid (DNA) template (T1) comprising contacting (T1) with a binding agent comprising at least one small duplex DNA-binding molecule (T2) coupled to at least one other small duplex binding molecule that binds to a non-overlapping region of target sequence (TS). The method is useful for inhibiting transcription of a range of disease-related genes for treating infections (by viruses, including human immunodeficiency virus, bacteria, fungi, protozoa and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Decreasing transcrip
cancer, by administr
regions of the gene.
                                                                                                                               Sequence 49 BP; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-)
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10
                               7 GGGGCCTGGCCCCTTAATA 25
                                                                16;
                                                                                Similarity
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GGGGCCCGGCCCGTTAAGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcriptional activity of genes for treating infections or administration of an agent that binds to two non-overlapping
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cantor CR,
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93US-00171389.
95US-00482080.
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92US-00996783
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                                                                                  14.2;
No. 3
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